

Science

Covid-19 may have been infecting humans since 2013: Study

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As the study around the coronavirus paces up, scientists have come up with another theory that the virus genome may have been spreading amongst the human population since 2013. However, the variant may have been evolved over the years, according to scientists at the University of Calgary, Canada.

The paper delved deeper into the possible origins of SARS-CoV-2 and how much of a role ACE-2 receptors play in making the virus infectious. The findings of the study are currently available in the preprint server Biorxiv, and the study hasn't been peer-reviewed yet.

According to the study, the virus takes time to mature and manifest into a more deadly form. However, the microorganisms could still be highly virulent and infectious in humans in the early stage.

It was found by a team of researchers early in January that the virus are present in bats. However, bats have already developed immunity against the virus to keep it in check. But, the same is not the case with humans. As a result, humans are susceptible to falling sick.

The study analyzed the current variant of the spike protein of SARS-CoV-2 and how strongly it binds to the ACE-2 receptor in humans (hACE-2). The binding between the spike protein of the novel coronavirus and the ACE-2 receptors on body cells is what helps the virus enter into healthy cells.

For the study, the researchers at the University of Calgary studied 479 genome sequences of the novel coronavirus gathered between 30 December 2019, and 20 March 2020. The sequence was used to discern its phylogeny — meaning the evolutionary development of the virus and relation to other closely related viruses.

Out of all the genomes, the researchers found about 16 variants of the virus and about 11 missense mutations (where a single nucleotide change makes the DNA/RNA to code for a different protein) in more than 5 per cent infections, each making their own phylogenetic tree.

Another one of their initial findings was the similarities with the bat and pangolin coronavirus. The genome of SARS-CoV-2 has been found to have at least 96 per cent similarity to a bat coronavirus — RaTG13 — and about 90 per cent to a pangolin coronavirus (Pangolin-CoV). It was previously suggested that the current virus is a combination of both these viruses that got created due to a co-infection in a host.

To study the origins, the researchers tried to create the ancestral sequence of the receptor-binding domain of the spike protein of SARS-CoV-2. The receptor-binding domain is the part of the spike protein that actually identifies and binds with the ACE-2 receptors. They created a common ancestral RBD sequence for all SARS-COV-2 viruses and labelled it N1 and its common ancestor with the closest animal virus — labelled N0 (N-Zero).

The discovery includes:

The N1 sequence was the same as that of the reference sequence from the SARS-CoV-2 virus, as expected, while the N0 sequence was unique, pointing to the unique origin of the virus.

The two RNA/DNA sequences only differ at four positions.

The ancestral sequence gave rise to various descendants, and the RaTG13 is one of the closest relatives of the SARS-COV-2 virus. Since the RaTG13 was found around 2013, the original ancestor of the COVID-19 causing virus must have been around at that time as well.

Interestingly, the earlier variants of the virus bound much more strongly to hACE2 than the recent one.

Conclusion

It is possible that the ancestor of the virus could have been infecting humans for a while but with fewer symptoms.

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